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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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45	44	43	42	41	40	9	38	37	36	35	34	33	32	31	30	29	28	27	26	25
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94.8	94.8			94.9		94.9	94.9	94.9	95.1	95.2	95.4	95.4	96.2				96.8	7	97.6	97.6
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Ade52800 Human apo	Ade52819 Human apo	Ade52802 Human apo	Ade52818 Human apo		Ade52798 Human apo	Aau98749 Chicken a	Aau98746 Chicken a	Aau98748 Chicken a	Aau98745 Chicken a		Ade52805 Human apo	Ade52808 Human apo	Aau98747 Chicken a	Ü		HIV TAT		Aau98757 Chicken a		Aay72943 CAV hexah

ALIGNMENTS

Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; mutein; cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bc1-2; gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-ab; mutant; Bc1-2-associating protein; BAG-1; cell proliferation disorder; alanine scanning; phosphorylation. AAU98752 standard; peptide; 121 AA. 20-OCT-2000; 2000EP-00203652. 20-OCT-2000; 2000US-0242397P. 19-OCT-2001; 2001WO-NL000771 Synthetic. Chicken anemia virus apoptin T108A mutant. 27-AUG-2002 AAU98752; Noteborn MHM, 25-APR-2002. Misc-difference Chicken anemia virus. WO200232954-A2. (LEAD-) LEADD (first entry) B۷. Rohn JL, Location/Qualifiers /note= "Wild-type Thr substituted by Ala" Mumberg 'n Donner

Aau98754 Aau98753

Aau98755

CTAV prot Chicken a Chicken a Chicken a

apopt

The invention relates to an isolated or recombinant phosphorylated Apoptin (I) also known as VP3 or its functional equivalent and/or functional fragment. Apoptin induces apoptosis in human malignant

ent and/or its malignant and

Disclosure; Page; 62pp; English.

Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells cancer prone cells, and for treating cancer or autoimmune disease.

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WPI; 2002-463306/49.

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RESULT 2
AAU98742
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Best Local Similarity
                                                                                                                                                                                                                                                                                                Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; mutein; cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bc1-2; gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant; Bc1-2-associating protein; BAG-1; cell proliferation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken anemia virus synthesised apoptin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU98742 standard; peptide; 121
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WO200232954-A2.
                                                                                                   Misc-difference
                                                                                                                                                                                                       Synthetic.
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                                                                                                   Location/Qualifiers
                                                                /note= "Wild-type Lys substituted by Arg"
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99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc chemotherapeutic agents inducing p53/Bcl-2 associated apoptions. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be cphosphorylated and a nucleic acid encoding a kinase capable of cphosphorylating apoptin, a gene delivery vehicle comprising the vector, a nost cell comprising the vector or vehicle, an anti-apoptin antibody, a cucleic acid encoding the antibody, a vector comprising the antibody concleic acid, a host cell comprising the antibody nucleic acid or vector, a nucleic acid, a host cell comprising the antibody nucleic acid or vector, a nucleic acid, a host cell comprising the antibody nucleic acid or vector, a poptin is useful for diagnostic purposes, for detecting the presence of cancer cells or cells that are cancer prone, for identifying a putative cancer relia or cells, and for identifying a tumour specific kinase. Compositions comprising the apoptins and antibodies are useful for kinase. Compositions comprising the apoptins and antibodies are useful for the selective destruction of tumour cells or hyperplasia, metaplasia or the selective destruction of tumour cells or hyperplasia, metaplasia or concentration and antibodies and cannot be blocked by Bcl-2, Bcr-abl or the Bcl-2-associating protein BAG-1. The present concentration is a synthesised apoptin containing a Lys to Arg mutation at constaining a Lys to Arg mutation at
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Matches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells cancer prone cells, and for treating cancer or autoimmune disease.
                                                                               ADE52796 standard; peptide; 121
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20-OCT-2000; 2000US-0242397P
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milarity 99.2%;
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Human apoptin

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; apoptin; NLS; nuclear localisation signal; aberrant-specific apoptosis; cytostatic; immunosu; cell proliferation; cancer; autoimmune disease.
            tumour-specific kinase; endogenous substrate; identification; kinase inhibitor; kinase modulator; cell proliferative disord apoptotic disorder; cancer; autoimmune disease; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fragment of Apoptin that induces aberrant-specific apoptosis, useful in preparing a medicament for treating a disease associated with enhanced cell proliferation or decreased cell death, e.g., cancer or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                              Apoptin; VP3;
                                                                                         Chicken anaemia virus (CAV)
                                                                                                                        20-MAY-2004
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cc characteristic or malignant and transformed cells (aberrant cells).

cc Apoptin is a small protein derived from chicken anaemia virus (CAV) which chiduces apoptosis in malignant and transformed cells, but not in normal cells. This pattern of apoptotic activity is related to the finding that the protein is phosphorylated on Thr 108 in aberrant cells, whereas it is not comportated at this position in normal cells, indicating that there is a tumour-specific kinase activity. The method of the invention aims to comport the following the time of the protein cells; incubating the components for this tumour-specific kinase could have been preparing lysates from aberrant and from normal reference could recognising phosphorylated Apoptin and phosphorylated substrate; and confidentifying the molecule, comparing the lysate components and identifying the substrate. The invention also relates to asubstrate obtained using the above method; a method of obtaining a modulator of a kinase involved in aberrant-specific Apoptin kinase; nucleic acids encoding the protein components and methods of selecting and identifying a molecule which binds to both aberrant cell-specific Apoptin and gene delivery vehicles comprising the components apoptin that is phosphorylated in aberrant cell-specific Apoptin and a cellular protein that is phosphorylated in aberrant cell-specific acids encoding the protein that is phosphorylated in aberrant cell-specific apoptin and a cellular protein that components and methods of selecting and identifying a molecule which binds to both aberrant cell-specific apoptin and a cellular protein that is phosphorylated in aberrant cell may be used to inhibit the confidence of a tumour-specific kinase towards its endogenous substrate and cellular protein cellular protein that its useful as a drug target for these disorders. The protein cellular is a disclosed as an inhibitor of an aberrant-specific cellular protein and according to the method of the protein cellular protein and according to the method of the compo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a substrate of a kinase capable of phosphorylating Apoptin in an aberrant-specific way, useful in inducing apoptosis in tumor cells, comprises preparing aberrant and reference cells and incubating with an
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A small proposis desired form the control of the control
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                                                                                                                                                                                                                         The invention relates to a method for identifying a substrate of a kinase capable of phosphorylating Apoptin (also known as VP3) in a manner characteristic of malignant and transformed cells (aberrant cells). Apoptin is a small protein derived from chicken anaemia virus (CAV) which induces apoptosis in malignant and transformed cells, but not in normal cells. This pattern of apoptotic activity is related to the finding that apoptin is phosphorylated on Thr 108 in aberrant cells, whereas it is not apoptin is phosphorylated on Thr 108 in aberrant cells, whereas it is not apoptin is phosphorylated on Thr 108 in aberrant cells.
   phosphorylated at this position in normal cells, indicating that there is a tumour-specific kinase activity. The method of the invention aims to identify endogenous cellular substrates for this tumour-specific kinase and involves preparing lysates from aberrant and from normal reference cells, incubating the components of the lysates with a molecule capable of recognising phosphorylated Apoptin and phosphorylated substrate; and visualising the molecule, comparing the lysate components and identifying visualising the molecule, comparing the lysate components and identifying the molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a substrate of a kinase capable of phosphorylating Apoptin in an aberrant-specific way, useful in inducing apoptosis in tumor cells, comprises preparing aberrant and reference cells and incubating with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-2003; 2003WO-NL000294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken anemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptin; VP3; CAV; tumour-specific phosphorylation; tumour-specific kinase; endogenous substrate; ident.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Page;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Noteborn MHM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-2002; 2002EP-00076596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptin loss-of-function mutant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-2004
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99.2%;
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Pred. No. 1.1e-60;
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                                                                                                                                                                                                                                                                                                                                                                                      a substrate of a kinase VP3) in a manner
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XX 19-J
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CC sequences ADM13010-ADM13011 represent loss-of-function Apoptin mutante which were used to demonstrate that the aberrant-specific Apoptin kinase considered to enset sequence is not shown in the specification, but was derived from the wild-type Apoptin sequence (ADM13007) and the information given on the wild-type Apoptin sequence (ADM13007) and the information given on the correction and the information given on the correction and the information given on the wild-type Apoptin sequence (ADM13007) and the information given on the correction and the inform
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Best Local S
Matches 120
                            WPI; 1995-075240/10
N-PSDB; AAQ82830.
                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken anemia virus VPI protein; apoptosis; cancer therapy; vaccine;
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19-AUG-1995
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                                                                                           Noteborn MHM,
                                                                                                                                                                                     20-JUL-1993;
                                                                                                                                                                                                                               19-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                   Chicken anemia virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VP3 protein.
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(first entry)
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Pred. No. 1.5e-60;
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Matches 119; Conservative
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                          The genome of the CIA-1 strain of chicken infectious anaemia virus encodes a VP-1 protein with at least four unique amino acid changes compared to the VP1 protein of other chicken infectious anaemia virus isolates. The new VP1 amino acid sequence exhibits a difference in pathogenic potential and cell tropism as compared to cell culture-adapted strains. New sequences (encoding VP1 (AAT10911), VP2 (AAT10912) and VP3
                                                                                                                                                                                                                                                                                                           Chicken infectious anaemia virus strain CIA-1 genome sequences, or VP1 sequence - useful to control chicken infectious anaemia such
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-087514/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1994;
03-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-1995;
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15-APR-1996
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                                                                                                                                                                                                                   Disclosure; Page 43-44; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORR ) CORNELL RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VP3 of chicken infectious anaemia virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR88499
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Pred. No. 2.4e-60;
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polypeptides may be used
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death, and for preventing or treating cancer and related proliferative disorders. (I) is also useful for studying mechanisms of carcinogenesis and metastases eukaryotic cells. (I) effectively transduces VP3 molecules directly into the cells. (I) attacks cancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be targeted by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents the CAV VP3 protein sequence which is given in the exemplification of the present invention
                                                                                                                                               The present invention describes a fusion molecule (I) comprising at le one protein transduction domain (PTD) and at least one chicken anaemic virus (CAV) VP3 molecule: (I) has cytostatic activity and can be used inducing cell death. (I) is useful for detecting cancerous or precancerous cells in a mammal or for killing or injuring cancerous to cancerous cells in a mammal. (I) is useful as a magnetic bullet to selectively kill cancer cells in vitro and in vivo, for inducing cell selectively kill cancer cells in vitro and in vivo.
                                                                                                                                                                                                                                                                                                               Novel fusion molecule useful for preventing a protein transduction domain and a chicken
                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-093056/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken anemia virus.
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                                                                                                                                                                                                                                                                                Page 22;
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Pred. No. 2.4e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein transduction domain;
proliferative cell disorder;
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Best Local Similarity
                                                                            The invention relates to an isolated or recombinant phosphorylated Apoptin (I) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for selective destruction of tumour cells which are resistant to
                                                                                                                                                                                                                                                                                                                        Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells cancer prone cells, and for treating cancer or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bcgene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant; Bcl-2-associating protein; BAG-1; cell proliferation disorder; alanine scanning; phosphorylation.
  chemotherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or functional equivalent and/or its functional fragment) which can be
                                                                                                                                                                                                                                                                      Disclosure; Page;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-463306/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Noteborn
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20-OCT-2000; 2000US-0242397P.
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                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mumberg
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    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Donner P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53; apoptosis; mutei
e; VP3; tumour; Bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT 10
AAU98759
ID 98759
IX AAU988759
AC AAU98
AC AAU98
AC AAU98
AC Chick
XX Immun
KW Cytoss
KW Gene
KW Gene
KW Bel-2
KW alani
XX Chick
OS Synth
XX Key
FT Misc-
F
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; mycottatic; autoimmune disease; immunosuppresesive; VP3; tumour; Bc. gene therapy; hyperplasia; metiaplasia; dysplasia; Bcr-abl; mutant; Bcl-2-associating protein; BAG-1; cell proliferation disorder; alanine scanning; phosphorylation.
                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken anemia virus apoptin T106A/T108A mutant.
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                                                                                                               25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken anemia virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU98759 standard; peptide; 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                  /note= "Wild-type Thr
                                                                                                                                                                                                                                                                                                                                              note= "Wild-type Thr substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.7%;
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Pred. No. 3.2e-60;
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                                                                                                                                                                                                                                                                  substituted by Ala"
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19-OCT-2001; 2001WO-NL000771.

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RESULT 11
AAU98756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC transformed cell lines but not in untransformed cells, by a p53
CC independent mechanism. Apoptin is therefore a candidate therapeutic for gelective destruction of tumour cells which are resistant to chemotherapeutic agents inducing p53/BCl-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be composited and a nucleic acid encoding a kinase capable of phosphorylated and a nucleic acid encoding a kinase capable of compositions or cells comprising the vector or vehicle, an anti-apoptin antibody, a nucleic acid encoding the antibody, a vector comprising the vector, a host cell comprising the vector or vehicle comprising the presence of cancer cells or cells that are cancer prone, for identifying a putative cancer relia or cells that are cancer prone, for identifying a putative cancer relia or cells, and for identifying a tumour specific kinase. CC compositions comprising the apoptins and antibodies are useful for treating an individual carrying a disease where enhanced cell cor auto-immune disease. Apoptin is useful as a therapeutic compound for the selective destruction of tumour cells or hyperplasia, metaplasia or clysplasia. Apoptin has no toxic effect in in vivo treatment regimes and cor auto-immune disease. Apoptin is useful as a therapeutic compound for the selective destruction of tumour cells or hyperplasia, metaplasia or cor cor cor correction senior to toxic effect in in vivo treatment regimes and correct or mapping the phosphorylation sites in apoptin. Note: The present sequence is not shown in the specification but was created by the indexer using the information in figure 4 and the wild-type apoptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
27-AUG-2002
                                           AAU98756;
                                                                                   AAU98756 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-2000; 2000EP-00203652.
20-OCT-2000; 2000US-0242397P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptin (I) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-463306/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                              121 L 121
                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                              119;
                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                       L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                           TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                                                                                        MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                    TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLIATAPSRPRTAKRRIR
                                                                                                                                                                                                                                                                                                                                                                                                               MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
(first entry)
                                                                                   peptide; 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mumberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 623; DB 5;
Pred. No. 3.2e-60;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Chemotherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also circulded are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylating apoptin, a gene delivery vehicle comprising the vector, a compressing the vector or vehicle, an anti-apoptin antibody, a nucleic acid, a host cell comprising the vector or vehicle, an anti-apoptin antibody, a concer cells or cells that are cancer prome, for identifying a putative cancer inducing agent, for testing the invitro treatment effect of cancer-inducing agent, for testing the invitro treatment effect of capoptin on tumour cells, and for identifying a tumour specific kinase. Compositions comprising the apoptins and antibodies are useful for treating an individual carrying a disease where enhanced cell compositions comprising the apoptin as useful as therapeutic compound for cor auto-immune disease. Apoptin is useful as therapeutic compound for dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and conduces apoptosis in the absence of functional p53 and cannot be blocked by Bcl-2, Bcr-abl or the Bcl-2-associating protein BAG-1. The present sequence is an apoptin mutant created during an experiment for mapping the phosphorylation sites in apoptin. Note: The present sequence is not shown in the specification but was created by the indexer using the conformation in figure 4 and the wild-type apoptin protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated or recombinant phosphorylated Apoptin (I) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for selective destruction of tumour cells which are resistant to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells cancer prone cells, and for treating cancer or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bc gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant; Bcl-2-associating protein; BAG-1; cell proliferation disorder; alanine scanning; phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page; 62pp; English.
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20-OCT-2000; 2000US-0242397P
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Query Match
Best Local Similarity
Matches 119; Conserv

98.7%;

Score 623; DB 5; Pred. No. 3.2e-60; 1; Mismatches 1;

Length 121;

Indels

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Gaps

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Sequence

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RESULT 12
AAU98750
ID AAU98750
XX AAU98750
XX AAU98750
XX I Immu
KW Cytcol
KW Gene
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The invention relates to an isolated or recombinant phosphorylated Apoptin (I) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and C transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for selective destruction of tumour cells which are resistant to chemotherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylating apoptin, a gene delivery vehicle capable of phosphorylating apoptin, a gene delivery vehicle comprising the vector, a nucleic acid, a host cell comprising the antibody, a vector comprising the antibody, a nucleic acid, a host cell comprising the antibody mucleic acid, a host cell comprising the antibody the antibody not set of the presence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells cancer prone cells, and for treating cancer or autoimmune disease.
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2000US-0242397P.
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AAU98751
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AC AAU98
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KW Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 118;
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   WPI; 2002-463306/49.
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                                                         Noteborn MHM, Rohn JL,
                                                                                                                                                                                   20-OCT-2000; 2000EP-00203652.
20-OCT-2000; 2000US-0242397P.
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18; Conservative
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Pred. No. 8.7e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              induces apoptosis in the absence of functional p53 and cannot be blocked by Bc1-2, Bcr-abl or the Bc1-2-associating protein BAG-1. The present sequence is an apoptin mutant-created during an alanine scanning experiment for mapping the phosphorylation sites in apoptin. Note: The present sequence is not shown in the specification but was created by the indexer using the information in figure 4 and the wild-type apoptin
                                                                                carcinogenesis; metastasis; fusion
                                                                                                                  Cancer cell death; cancer; tumour; chicken anaemia virus; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 121
                                                                                                                                                                                                                                             TAT-VP3 fusion protein.
                                                                                                                                                                                                                                                                                                                              27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                   ABP56092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP56092 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic selective destruction of tumour cells which are resistant to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells cancer prone cells, and for treating cancer or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              functional fragment. Apoptin
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97.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 619; DB 5;
Pred. No. 8.7e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                            protein transduction domain; proliferative cell disorder; protein.
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Chicken anemia virus

WO200285305-A2

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RESULT 15
ABP56095
ID ABP56
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XX PTD4-FE
XX Cance
KW Chick
KW Chick
XW Chick
XW Chick
XX Synt!
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Best Local (
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                                                                                                                                              Cancer cell death; cancer; tumour; protein transduction domain; chicken anaemia virus; cytostatic; proliferative cell disorder; carcinogenesis; metastasis; fusion protein.
                                                                        Synthetic
                                                                                                                                                                                                                                                                                            27-FEB-2003
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                                                                                                 Chicken anemia
                                                                                                                                                                                                                                             PTD4-VP3
                                                                                                                                                                                                                                                                                                                                                                                      ABP56095 standard; protein; 190 AA
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                                                                                                                                                                                                                                             fusion protein.
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                                                                                                   virus.
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98.3%;
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Pred. No. 1.5e-59;
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Search completed: April 20, 2006, 12:13:06 Job time : 190 secs
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                                                                                                                                                                                                                                         Matches 118; Conservative
                                                                                                                                                                                                                                                       Query Match 98.1%;
Best Local Similarity 98.3%;
                                                                                                                                                                                                                                                                                                                     Sequence 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 36; Fig 5B; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel fusion molecule useful for preventing or treating cancer, comprises a protein transduction domain and a chicken anemia virus VP3 molecule.
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                                                                                                       ADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRRIFL 121
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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B39926
hypothetical protein 2 - chicken anemia virus
C;Species: chicken anemia virus, CAV
C;Species: chicken anemia virus, CAV
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Oct-2004
C;Accession: B39926
R;Noteborn, M.H.M.; de Boer, G.F.; van Roozelaar, D.J.; Karreman, C.; Kranenburg, O.; \
J. Virol. 65, 3131-3139, 1991
A;Title: Characcerization of cloned chicken anemia virus DNA that contains all elements
A;Reference number: A39926; MUID:91237831; PMID:1851873
A;Accession: B39926
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <NOT-
A;Cross-references: UNIPROT:Q99152; UNIPARC:UPI00000528A6; GB:M55918; NID:g323250; PIDN
C;Comment: This virus is unclassified.
C;Superfamily: apoptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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45	44	43	42 .	41	40	39	38	37	36	35	34	u u	32	31	30
70.5	70.5	70.5	71	71	71	71.5	71.5	72	72	72	72	72.5	72.5	72.5	72.5
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924	407	315	975	796	137	2187	1046	1622	1250	1232	298	929	913	486	416
Ŋ	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
A44945	T36204	A56561	T48107	JC7355	E72614	T30826	T29776	JE0378	T22845	S40766	AD3162	T52517	S20590	S47891	S27198
104K microneme-rho	hypothetical prote	35K proline-rich p	hypothetical prote	peroxisome prolife	hypothetical prote	nascent polypeptid	hypothetical prote	DNA (cytosine-5-)-	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	exo-alpha-sialidas	exuperantia protei	homeotic protein H

ALIGNMENTS

A;Accession: B48343 A;Molecule type: DNA A;Residues: 1-121 <mee> A;Residues: 1-121 <mee> A;Cross-references: UNIPROT:099152; UNIPARC:UPI0000170E18; GB:M81223; NID:g323254; PIDN A;Note: the authors translated the codon ACA for residue 41 as Gly A;Note: sequence extracted from NCBI backbone (NCBIN:106168, NCBIP:106170) C;Superfamily: apoptin</mee></mee>	RESULT 2 B48343 hypothetical 13K protein - chicken anemia virus (isolate Cux-1) C;Species: Chicken anemia virus, CAV C;Species: Chicken anemia virus (isolate Cux-1) C;Accession: B48343 C;Accession: B48343 C;Accession: B48343 R;Meehan, B.M.; Todd, D.; Creelan, J.L.; Earle, J.A.; Hoey, E.M.; McNulty, M.S. A;Ch. Virol. 124, 301-319, 1992 A;Title: Characterization of viral DNAs from cells infected with chicken anaemia agent: A;Reference number: A48343; MUID:92296898; PMID:1605740	121 L		Qy 1 MNALQEDTPPGDSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60	Query Match 98.9%; Score 624; DB 2; Length 121; Best Local Similarity 98.3%; Pred. No. 4.6e-52; Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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mucin 7 precursor, salivary - human
N;Alternate names: mucin, MG2; mucin, MG2a-T1; mucin, MG2a-T2; mucin, MG2b-T2
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48018; S29115; S29114
R;Bobek, L.A.; Tsai, H.; Biesbrock, A.R.; Levine, M.J.
J. Biol. Chem. 268, 2053-20569, 1993
A;Title: Molecular cloning, sequence, and specificity of expression of the gene encot A;Reference number: A48018; MUID:93388636; PMID:7690757
A;Accession: A48018
A;Molecule type: mRNA
A;Residues: 1-377 <BOB>
A;Cross-reference. The common of the concession of the gene encot A;Residues: 1-377 <BOB>
A;Cross-reference. The concession of the gene encot A;Cross-reference.
                                             A;Cross-references: UNIPROT:09UCD8; UNIPARC:UPI000003DBBB; GB:L13283 A;Experimental source: submandibular gland A;Note: sequence extracted from NCBI backbone (NCBIN:137719, NCBIP:1 R;Reddy, M.S.; Bobek, L.A.; Haraszthy, G.G.; Biesbrock, A.R.; Levine Biochem. J. 287, 639-643, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-247 <TIN>
A;Cross-references: UNIPROT:044145; UNIPARC:UPI00001793B3; EMBL:AF036692; PIDN:AAB88324
A;Experimental source: strain Bristol N2; clone C44B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Tin-Wollam, A.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C44B12.
A;Reference number: Z21183
A;Accession: T32514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C44B12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T32514
Biochem. J. 287, 639-643, 1992
A;Title: Structural features of the low-molecular-mass human salivary mucin
A;Reference number: S29114; MUID:93075006; PMID:1445223
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Similarity 97.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRRIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.3%; Score 84; DB 2; Length 247; 29.7%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                 NCBIP:137720)
                                                                                     Levine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pEARLI 4 protein [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: D84595
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F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-37/Product: mucin 7, salivary #status predicted <MAT>
F;97,128,135,146,312/Binding site:|carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 143-145,'X',147,'XXX',151-152,'X',154-158,'X',160-161,'A',163-164,'XX',167-
A;Cross-references: UNIPARC:UPI0000073BF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 'S',71-79,'N',81-86,'XX',89,'X',91,'P'
A;Cross-references: UNIPARC:UPI0000073BF7
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A;Molecule type: mRNA
A;Residues: 143-168 <RED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-748 <STO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:138799; OMIM:158375
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                                                                                                                                                                                                                                                                                                    Local
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    297
                                              116 RRRIR
                                                                                            238 RTPIHĖŠAATERRĖQTPETRĖRTĖ-EHRSAIĖDTRPRTPIHĖSAATGRRPQTPETRĖRTA
                                                                                                                                                                                       199 DTRPRTPIHESAATGRRP-QTPETR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 ---SAPPETTAAPPTPSATTPAPPSSPAPQETTAAPITTPNSSPTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 PTPPATTPAPPSSSAPPETTAAPPTPSATTPAPLSSSAPPETTAVPPTPSATTLDPSSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 GFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRT 114
                                                                                                                                           65 ----SESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLIT----TAPSRPRTA
                                                                                                                                                                                                                                7 DTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADN--
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31; Conservative
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    301
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Pred. No. 2.3;
8; Mismatches
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                                                                                                                                                                                                                                                                                                       Score 80.5;
Pred. No. 8.
                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                               Length 748;
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R;Johnson, D.
submitted to the EMBL Data Library, May 1997
submitted to the sequence of C. elegans cosmid F59E12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-1082 <JOH>
A;Residues: 1-1082 <UHPI000017BA57; EMBL:AF003386; NID:g2088833; PID:g2088836; PI
A;Experimental source: strain Bristol N2; clone F59E12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F59E12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70752
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C;Species: Mycobacterium tuberrulosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: CESP:F59E12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference number: Z18318
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Best Local (
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                                                                                                                                                                                                                                                                 9 PPGPSTVFRPPTSSR-PLETPHCR----EIRI----GIAGITITLSLCGCANARA---
                                                                                                                                                                                                                                                                                                            36;
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                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                    RTA-----RRR 118
                                                                                                                                            PRIHSSASKKTEKPETPRAESPD-
                                                                                                                                                                                PTLRSATADNSE--STGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRP 112
                                                                                                                                                                                                                           PASPKAISHPSTPAKSPQKTPQKKKEITPVEVKIEEIKEEEDVTPSQSPPATQTPRSRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRP 112
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                                                             RISTVVPMITERE 664
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ilarity 27.2%;
Conservative
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                             12.6%; Score 79.5;
27.1%; Pred. No. 1
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Pred. No. 2.2;
11; Mismatches
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                                                                                                                                                                                                                                                                                                            46; Indels
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A; Introns: 52/1; 314/3;
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                                                                                                                                                                                                                                                                   A; Gene: CESP: M01E11.6
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A; Residues: 1-475 <STO>
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                     70
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35; Conserv
                                                                                                                                                                   Similarity
FKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRP
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RESULT

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protein F22G5.18 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Accession: D86209 C;Accession: D86209 C;Accession: D86209 R;Theologis, A.; Ecker, J.R.; Palm', C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K ansen, N.F.; Hughes, B.; Huizar, L. Alauthors, Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial: C.A.; Li, J.R.; Cony, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: D86209
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-587 <PAU>
                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, November 1996 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 15-Oct-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein M01E11.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                      ;Cross-references: UNIPROT:P91400; UNIPARC:UP100000809D5; EMBL:U80450; PIDN:AAB37830.:
;Experimental source: strain Bristol N2; clone M01E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 TLSLCGCANARAPTLRSATADNSESTGFKNVPDLRTDQPKP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SSAQKPTPGGPLTHDLNVPYEGTEEYETPTAEMLFPPT---PLQTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NALQEDTPPGPST-----
PERSAMAKPASCSRPI-
                                                       PGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNSESTG
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                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                     460/1
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23.3%; Pred. No. 7.
                                                                                                                                12.4%; Score 78.5; I
23.3%; Pred. No. 9.7;
cive 12; Mismatches
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                                                                                                                                Indels
   PTMQSTASRISTLTA 105
                                                                                                                                    29;
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C; Date: U3-PM, S38148
C; Accession: S38148
R; Pohl, T.M.; Pohl, F.M.
submitted to the Protein Sequence Database, Ma
A; Reference number: S37897
A; Accession: S38148
A; Molecule type: DNA
A; Residues: 1-348 < POH>
A; Residues: 1-348 < POH>
A; Residues: UNIPROT: P36152; UNIPARC: U
           N;Alternate names: neuroglycan
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A41558; S18866
R;Carey, D.J.; Evans, D.M.; Stahl, R.C.; Asundi, V.K.; Conner, K.J.; Garbes
J. Cell Biol. 117, 191-201, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N,Alternate names: MC158R
C;Species: Mclluscum contagiosum virus 1
C;Species: Mclluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T30760
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, Science 273, 813-816, 1996
A; Title: Molecular cloning and characterization of N-syndecan,
                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                   RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Saccharomyces cerevisiae;Date: 03-May-1994 #text_change;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change
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Best Local &
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Similarity 33.3%;
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                                                                                                                                                                                                                                                                                                                                         PGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNSESTG 69
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                                                                                                                                                                                                                             TPEOPSLSPSPPPPP
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Pred. No. 4.2;
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Pred. No. 7.7;
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   a novel transmembrane
                                     K.J.; Garbes,
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A;Cross-references: UNIPROT:P09027; UNIPARC:UPI0000026946; R;Tan, D.P.; Shao, X.; Pu, L.; Guo, V.; Nirenberg, M. Proc. Natl. Acad. Sci. U.S.A. 93, 8247-825; 1996. A;Title: Sequence and expression of the marine. Hoxd-3 homeo A;Reference number: JC6144; MUID:96323206; PMID:8710855 A;Contents: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 27-Jan-1995 #text_change
C;Date: 27-Jan-1995 #text_change
C;Date: 27-Jan-1995 #text_change
C;Date: 27-Jan-1995 #text_change
C;Accession: S47539; JC6144
R;Brown, W.M.; Zhou, L.; Taylor, G.R.
Biochim. Biophys. Acta 1219, 219-222, 1994
A;Title: The nucleotide sequence of the murine Hox-D3 (Hox-4.1)
A;Reference number: S47539; MUID: 94368862; PMID: 7916214
                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: homeotic protein Hox B3; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription F;180-236/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI0000026946; GB:U56400; C;Comment: This protein is a homeodomain protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-417 < TAI
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A; Residues: 1-417 < BRO>
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A; Residues: 1-353 < CAR>
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290 S-QPNMYGLAAYTAPLSSCLPQQKR 313
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                                             89 SCDPSEYRVSELKESLITTAPSRPR 113
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                                                                                                                                                42 -----ITLSLCGCANARAPTLRSATADNSESTGFKNVPDLRTDQPKPPSKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 TLRSATADNSESTGFKNVP-----DLRTD-----
                                                                                                                                                                                                                                                      5 QEDTPPGPST--VFRPPTSSRPLETPH-----CREIRIGIAGIT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   names: homeobox-containing protein Hox-4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-417 <TAN>
                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                   RRMKYKKDQKAKGILHSPAGQSPERSPPLGGAAGHVAYSGQLPPVPGLAYDAPSPPAFAK
                                                                                                                                                                                                   EDKSPPGPASKRVRTAYTSAOLVELEKEFHFNRYLCRPRRVEMANLLNLTEROIKIWFQN
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                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                         Score 76.5; D
Pred. No. 10;
21; Mismatches
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R;Fenger, U.; Hofmann, M.; Galliot, B.; Schaller, H.C. submitted to the EMBL Data Library, June 1994
A;Description: The role of the cAMP pathway in mediating the effect of head activator on A;Reference number: S47091
A;Accession: S47091
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A;Introns: 52/1; 314/3; 460/1
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C;Superfamily: adenylyl cyclase-associated protein MCH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cyclase-associated protein - Chlorohydra viridissima
C.Species: Chlorohydra viridissima
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
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S47091
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submitted to the EMBL Data Library, October 1996
A;Reference number: Z19192
A;Accession: T19893
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 24.7
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ypothetical protein C41G7.2 - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ;Molecule type: DNA;Residues: 1-587 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                     Gene: CESP:C41G7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:Q93366; UNIPARC:UPI0000060F51; EMBL:Z81048; PIDN:CAB02839.1; Experimental source: clone C41G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Status: preliminary
;Molecule type: mRNA
;Residues: 1-481 <FEN>
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  126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 VSAHKPPVPPPPSGFAPPPPP--PIQAP----
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                                                                                                                                 51 NARA----
                                                                                                                                                                                                                       13 STVFRPPTSSR------CA 50
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Similarity 24.8%; Pred. No. 12;
                                                                                     TGRASLPERSAMAKTSTSSHSRPALOSTASRNTTLTAASTSROLRTGRPPPPSTORS--- 125
                                                                                                                                                                                STIGAPPKATRGRAAAPPIKEADPATIP--ROSAPG--GITIGAAACRPPSRLPGATISA 68
                                              SEYRVSELKESLITTAPSRPRTARRR 118
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Submitted (OCT-2002) to the EMBL/denBank/DDBJ da

EMBL; AF390102; AAM73651.1; -; Genomic_DNA.

EMBL; AY171617; AA045416.1; -; Genomic_DNA.

GO; GO:00142025; C:host cell nucleus; IEA.

GO; GO:0019051; P:induction of apoptosis by viru

InterPro; IPR006858; CAV VP3.

Pfam; PF04771; CAV VP3.

SEQUENCE 121 AA; 13298 MW; DZAAB3869BD61A3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VP3 (Apoptin).
Name-Np3;
Chicken anemia virus.
Viruses; ssDNA viruses; (NCBI TaxID=12618;
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PubMed=14648297; DOI-10.1007/800705-003-0189-3;
PubMed=15648297; DOI-10.1007/800705-003-0189-3;
Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
Md-Zain B.M., Kono Y.;
Md-Zain B.M., Kono Y.;
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10-MAY-2005
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1: FUNCTION: May act as transcriptional regulator. Induces agent in infected cells. Element of infectious replication cycle.: SUBCELLULAR LOCATION: Nuclear; nucleus of infected cells.
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Noteborn M.H.M., de Boer G.F., van Roozelaar D.J., Karreman C.,
Kranenburg O., Vos J.G., Jeurissen S.H.M., Hoeben R.C., Zantema A.,
Koch G., van Ormondt H., van der Eb A.J.;
"Characterization of cloned chicken anemia virus DNA that contains
elements for the infectious replication cycle.";
J. Virol. 65:3131-3139(1991).
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EMBL; M81223; AAA42883.1;
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Viruses; ssDNA viruses; Circoviridae;
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MEDLINE=98001356; PubMed=9343191; Meehan B.M., Todd D., Creelan J.L., Connor T.J., McNulty M.S.; "Investigation of the attenuation exhibited by a molecularly cichicken anemia virus isolate by utilizing a chimeric virus app. J. Virol. 71:8362-8367(1997).
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Scott A.N.J., McNulty M.S., Todd D.;
"Characterisation of a chicken anaemia virus variant population that resists neutralisation with a group-specific monoclonal antibody.";
Arch. Virol. 146:713-728(2001).
EMBL; AJ297682; CAC14758.1; -; Genomic DNA.
GO; GO:0019051; Chost cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR006858; CAV VP3.
Pfam; PF04771; CAV VP3; I.
SEQUENCE 121 AA; 13284 MW; 82ABB3865CCBACE5 CRC64;
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                                                                                        "Molecular cloning of an attenuated chicken following repeated cell culture passage."; Avian Pathol. 24:171-187(1995).
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McKenna G.F.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

NUCLEOTIDE SEQUENCE

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Matches 119; Conser
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01-OCT-1996
30-MAY-2000
10-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptin (VP3).
Chicken anemia virus (isolate USA CIA-1) (CAV).
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
NCBI_TaxID=73478;
                                                    EMBL; L14767; AAD09423.1; -; G
InterPro; IPRO6855; CAV VP3.
Pfam; PP04771; CAV VP3; I.
Apoptosis; Nuclear protein.
SEQUENCE 121 AA; 13245 MW;
                                                                                                                                                                                                                                                                                                                       Renshaw R.W., Soine C., Weinkle T., O'Connell P.H., Ohashi K., Watson S., Lucio B., Harrington S., Schat K.A.; "A hypervariable region in VP1 of chicken infectious anemia virus mediates rate of spread and cell tropism in tissue culture."; J. Virol. 70:8872-8878 (1996).
                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatice Institute. There are no restruse as long as its content is in no way modified and this s
                                                                                                                                                                                                                         Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: May act as transcriptional regulator. Induces apoptosis in infected cells. Blement of infectious replication cycle.

-:- SUBCELLULAR LOCATION: Nuclear; nucleus of infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U66304, AACS8477.1; -; Genomic DNA.
EMBL; AJ536295; CAD60259.1; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPRO06858; CAV VP3.
Pfam; PF04771; CAV VP3.
121 AA; 13312 MW; E4AAB75960F2C5C5 CRC64;
                                                                                                                                                                                                                                                                                Renshaw R.W
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                                                                                                                                                                                                                                                                                               SEQUENCE REVISION TO 50.
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les 119; Conservative
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39, Last sequence up
47, Last annotation
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Score 619; DB 1;
Pred. No. 1.3e-49;
0; Mismatches 2
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0; Mismatches 2
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Best Local Sim
Matches 119;
NUCLEOTIDE SEQUENCE.
MEDLINE=21296594; PubMed=11402858; DOI=10.1007/s007050170141;
Scott A.N.J., McNulty M.S., Todd D.;
                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                             Q9DWX3_9CIRC PRELIMINARY;
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Scott A.N.J., McNulty M.S., Todd D.;
"Characterisation of a chicken anaemia virus variant population that resists neutralisation with a group-specific monoclonal antibody.";
Arch. Virol. 146:713-728(2001).
EMBL; AJ297683; CAC14761.1; -; Genomic DNA.
EMBL; AJ29769; CAC14749.1; -; Genomic DNA.
EMBL; AJ29769; CAC14752.1; -; Genomic DNA.
EMBL; AJ297680; CAC14752.1; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR006859; CAV VP3.
Pfam; PF04771; CAV VP3.
11 EAV VP3.
12 EAV VP3.
13272 MW; 33EFA7D7CA93013F CRC64;
                                                                                                                                      Viruses; ssDNA
                                                                                                                                                                                                             VP3 protein.
                                                                                                        NCBI_TaxID=12618;
                                                                                                                                                         Chicken anemia virus.
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NCBI_TaxID=12618;
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Pred. No. 1.3e-49;
D; Mismatches 2;
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Best Local Sim
Matches 119;
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01-OCT-2003
13-SEP-2005
 Submitted [6]
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21310375; PubMed=11417817; Van Santen V.L., Li L., Hoerr F.J., L "Genetic characterization of chicken broiler chickens in Alabama."; Avian Dis. 45:373-388(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chicken anemia virus.
Viruses; ssDNA viruses;
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Q91N81;
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EMBL; AJ297681; CAC14755.1; -; Genomic_DNA.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0019051; P:induction of apoptosis by virus;

InterPro; IPR006858; CAV_VP3.

Pfam; PF04771; CAV_VP3.

121 AA; 13329 MW; A471DFF69BD61A3F CR0
                              STRAIN=Delrose;
                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.

van Santen V.L., Toro H.,
Submitted (JUL-2003) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterisation of a chicken anaemia virus variant population that resists neutralisation with a group-specific monoclonal antibody.";
                                                              NUCLEOTIDE SEQUENCE
                                                                                         anaemia virus.
J. Gen. Virol.
                                                                                                                                                   MEDLINE=21195622; PubMed=11297698;
Yamaguchi S., Imada T., Kaji N., Mase M.,
                                                                                                                                                                                  STRAIN=AH9410
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                                                                                                                                        Yuasa
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                                                                                                                       "Identification of a genetic determinant
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98.3%;
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    EMBL; AF475908; AAL79914.1; EMBL; AF520788; AAM75347.1; EMBL; AY839944; AAW02946.1; EMBL; AY843527; AAW30191.1; EMBL; AY999018; AAY15241.1; GO; GO:0042025; C:host cell n GO; GO:0019051; P:induction o
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EMBL;
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Jadhao S.J., Pattnaik B
Submitted (JUN-2002) to
      SEQUENCE
                   InterPro; IPR006858; CAV
Pfam; PF04771; CAV_VP3; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=LF4;
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Kono Y.;
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Toshniwal R.M., Dash ne EMBL/GenBank/DDBJ o

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Pradhan H.K.;

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CAV_VP3;

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AAK54239 AAG34178.

Genomic DNA

BAB19645. BAB19642 BAA90490 AAK70849.

Genomic DNA.
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Chowdhury S....
Kono Y., Darus A.;
Kono Y., Darus A.;
NUCLEOTIDE SEQUENCE.
He C.Q., Li Y.L.;
Submitted (JAN-2002)
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                                                       Submitted (JUN-2001)
                                                                                 NUCLEOTIDE SEQUENCE Chowdhury S.M.Z.H.,
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Spackman E., Rosenbe
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low and high p
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AC Q75ZF9;
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DT 05-JUL-2004 (Tremblrel. 27,
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Best Local Similarity
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ.

EMBL; AY040632; AAK82947.1; -; Genomic_DNA.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0019051; P:induction of apoptosis by vi
InterPro; IPR006858; CAV_VP3.

Pfam; PF04771; CAV_VP3; I.

SEQUENCE 121 AA; 13338 MW; CD34CA7E9BD61A:
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Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin
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PubMed=14648297; DOI=10.1007/800705-003-0189-3;
PubMed=14648297; DOI=10.1007/800705-003-0189-3;
Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
Md-Zain B.M., Kono Y.;
Md-Zain B.M., Kono Y.;
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Viruses; ssDNA viruses;
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01-OCT-2002
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QBJNK4;
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Pred. No. 1.3e-49;
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NUCLEOTIDE SEQUENCE.

MEDILYMS=21296594; PubMed=11402858; DOI=10.1007/8007050170141;

Scott A.N.J., McNulty M.S., Tödd D.;

"Characterisation of a Chicken anaemia virus variant population resists neutralisation with a group-specific monoclonal antibody Arch. Virol. 146:713-728 (2001).

EMBL; AJ297686; CaC14770.1; -; Genomic DNA.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0019051; P:induction of apoptosis by virus; IEA.

InterPro; IPR006858; CAV VP3.

Ffam; PF04771; CAV VP3; I

SEQUENCE 121 AA; 13240 MW; D7ABB05D37A61A3E CRC64;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ABI19448; BAD12197.1; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019051; F:induction of apoptosis by virus; IEA.
InterPro; IPR006858; CAV VP3.
Pfam; PF04771; CAV_VP3; I.
SEQUENCE 121 AA; 13272 MW; DA0822253B28FAD0 CRC64;
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01-MAR-2001 (TrEMBLrel.
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Viruses; ssDNA viruses;
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Name=VP3;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB027470; BAA77833.1; -; Genomic DNA.
EMBL; AF395114; AAM20898.1; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR006858; CAV VP3.
Pfam; PF04771; CAV VP3; 1.

SEQUENCE 121 AA; 13272 MW; 72B7AE9C2BD60EB8 CRC64;
                                        Chicken anemia virus.
Viruses; ssDNA viruses;
NCBI_TaxID=12618;
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the EMBL/GenBank/DDBJ
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Submitted (JUL-2003) to the EMBL/GenBank/DDI
EMBL; AF311992; AAK70835.2; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:019051; F:induction of apoptos1s by
InterPro; IPR006858; CAV VP3.
Pfam; PF04771; CAV VP3.
SEQUENCE 121 AA; 13231 MW; B4AAB39C2DD6:
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InterPro; IPR006558; CAV VP3.
Pfam; PF04771; CAV_VP3; I.
Apoptosis; Nuclear protein.
SEQUENCE 121 AA; 13233 MW;
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Chicken anemia virus (isolate Japan 82-2) (CAV).
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
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    -I- FUNCTION: May act as transcriptional regulator. Induces at
in infected cells. Element of infectious replication cycles.
    -I- SUBCELLULAR LOCATION: Nuclear; nucleus of infected cells.

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Kato A., Fujino M., Nakamura T., Ishi
"Gene organization of chicken anemia
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"Genetic characterization of chicken
broiler chickens in Alabama.";
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ne EMBL/GenBank/DDBJ
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Cardona C.J., Oswald W.B., Schat K.A.;
Cardona C.J., Oswald W.B., Schat K.A.;
"Distribution of Chicken anaemia virus in the reproductive tissues of specific-pathogen-free chickens.";
J. Gen. Virol. 81:2067-2075 (2000).
EMBL; AR214563; AAF37220.1; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR006858; CAV_VP3.
Pfam; pF04771; CAV_VP3; I.
SEQUENCE 121 AA; 13215 MW; 22AAB38D3ACBB153 CRC64;
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Perfect score:
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US-09-645-415A-58
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US-09-652-991A-25918
US-09-252-991A-25918
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ALIGNMENTS

and

PRIOR APPLICATION DATA: APPLICATION NUMBER: NI 9002008 FILING DATE: 12-SEP-1990 ATTORNEY_AGENT INFORMATION: NAME: RAE-VENTER, BARBARA REGISTRATION NUMBER: 32,750 REFERENCE/DOCKET NUMBER: 12BBV.003.04US TELECOMMUNICATION INFORMATION: TELESPHONE: (650)328-4400	PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/NL 94/00168 FILING DATE: 19-JUL-1994 PRIOR APPLICATION DATA: RAPPLICATION DATA: APPLICATION NUMBER: PCT/NL 91/00165 FILING DATE: 11-SEP-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: NL 9301272 FILING DATE: 20-JUL-1993	COMPUTER: IEAD C COMPUTER: PATENTION PC-DOS/MS-DOS SOFTWARE: PATENTION PATA: SPELICATION UNMER: US/08/489,666C PILING DATE: 07-JUN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/454,121 FILING DATE: 30-NOV-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/454,121 FILING DATE: 30-NOV-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/030,335 PRIOR DATE: 08-MAR-1993	TION: Chicken Anemia Virus mutants and TION: vaccines and uses based on the viral proteins VP1, TION: vaccines and uses based on the viral proteins VP1, TION: VP3 or sequences of that virus coding therefor. ENCES: 30 ADDRESS: SHERIDAN AVE., P.O. BOX 60039 ALTO BLE FORM:
			VP2

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Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
FILING DALL.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL91/00165
APPLICATION NUMBER: 11-SEP-1991
                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL94/00168
FILING DATE: 19-UULY-1994
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
PILING DATE: 30-NOV-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US/08/911,092
PILING DATE: 14-AUG-1997
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                                                                                                        FILING DATE: 20-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/030,335
FILING DATE: 8-MAR-1993
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Pred. No. 2.4e-65;
1; Mismatches 1
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Best Local Similarity 98.3
Matches 119; Conservative
                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
PRIOR APPLICATION DATA:
30-NOVEMBER-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL94/00168
PILING DATE: 19-JULY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/030,335
APPLICATION NUMBER: US 08/030,335
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                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,001B
FILING DATE: 07-UNE-1995
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
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              ING DATE: 8-MARCH-1993
APPLICATION DATA:
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                                                                                                      PCT/NL94/00168
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NL 9301272
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    Mismatches

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Pred. No. 2.4e-65;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

20-JULY-1993

FILING DATE:

11-SEPTEMBER-1991

PCT/NL91/00165

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Matches 119;
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Best Local Similarity
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TELEFAX: (650) 424-8760
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equence 7, Application US/08454121A
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: No. 607153
APPLICANT: Koch, Guus
TITLE OF INVENTION: 0
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,121A
FILING DATE: 07-JUNE-1995
                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL94/00168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
PILING DATE: 19-JULY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 93
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                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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REFERENCE/DOCKET NUMBER: LEBV.003.02US
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O. Box 60039
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And Uses Based On The Viral Proteins VP1,
Sequences Of That Virus Coding Therefor
 NL 9301272
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Pred. No. 2.4e-65;
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US-08-454-121A-7
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Koch, Guu
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              FILING DATE: 07-JUNE
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: No. 6162461eborn, Matheus H.M. APPLICANT: Koch, Guus
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
                                                                                         CURRENT APPLICATION DATA: US
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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LENGTH: 121 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
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APPLICATION NUMBER: US 08/454,121 FILING DATE: 30-NOVEMBER-1995
                                                                                                                                                                                                                                                           STREET: P.O. Box 60039
CITY: Palo Alto
STATE: California
                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                          COUNTRY: USA
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FILING DATE: 11-SEP-1991
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8-MAR-1993
                                                                         07-JUNE-1995
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                                                                                                                                                                                                                                                                                                                                                                      Sequences Of That Virus Coding Therefor
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                                                                                         US/08/482,161B
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Pred. No. 2.4e-65;
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Best Local Similarity 98.3%;
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 424-8760 NFORMATION FOR SEQ ID NO: '
                             SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                   APPLICANT:
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HYPOTHETICAL:
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REFERENCE/DOCKET NUMBER: LEBV.003.01US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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APPLICATION NUMBER:
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                 APPLICATION NUMBER:
                                                                                                                                                                               CITY: PALO ALTO
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                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                 ADDRESSEE:
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o. 6217870
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09-APR-1998
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            US/09/057,963A
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Pred. No. 2.4e-65;
1; Mismatches 1
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Best Local Similarity
Matches 119; Conserv
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APPLICANT: Lin, S.
APPLICANT: Belcourt, M.
APPLICANT: Belcourt, M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
FILE REFERENCE: 8002-059
CURRENT APPLICATION NUMBER: US/09/645,415A
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/157,581
                                                                                                                                                                                                                         Patent No.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NOWBER: NL 9301
FILING DATE: 20-JHL-1007
PRIOR ADDITE: 20-JHL-1007
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FILING DATE: 12-SEP-1990
ATTORNEY/AGENT IMFORMATION:
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PRIOR APPLICATION DATA:
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STRANDEDNESS: not
TOPOLOGY: not rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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6962696
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Clairmont, C.
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Pred. No. 2.4e-65;
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SEQ ID NO 60
LENGTH: 140
TYPE: PRT
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PRIOR APPLICATION NUMBER: 60/157,637
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 58
LENGTH: 134
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                                                                                                                                                                                                                Matches
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ORGANISM: Bacteriophage
-09-645-415A-58
                                                                                                                                                                                                                                                                                 ORGANISM: Bacteriophage
-09-645-415A-60
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                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/157,581
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: 60/157,637
PRIOR FILING DATE: 1999-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/645,415A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 8002-059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Belcourt, M.
IITLE OF INVENTION: COMPOSITIONS AND METHODS
IITLE OF INVENTION: TUMOR-TARGETED DELIVERY
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140 L 140
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                                                                       TADNSENTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRCIR 139
                                                                                                         TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRRIR 120
                                                                                                                                          MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
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Pred. No. 2.6e-64;
1; Mismatches 2
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Pred. No. 2.4e-64;
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RESULT

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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 259.8
LENGTH: 757
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Best Local S
Matches .37
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Matches
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. RUBENFION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 30531
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION STATE 
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TITLE OF INVENTION:
TITLE OF INVENTION:
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 488
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112 PR 113
                                                                        49 SADSSEDTRGRDFGGDGDQQRRHLR-DQPSPTVSTAYSCSAS----AVLRPFCVTPMAMP 103
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                                                                                                                                                    61 TADNSEST
                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
.37; Conserv
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36; Conserv
                                                                                                                                                                                                                                PP-----PPTSS-----ARARKVRVGTPGIRPNSTSNRPPISSALGCATTCSPMSLPR 48
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                                                                                                                                                                                                                                                                                                                                                                         13.5%; Score 85; DB 2; Le llarity 30.3%; Pred. No. 0.21; Conservative 10; Mismatches .41;
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA: FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                        GFKNVPDLRTDQPKPP-SKKRSCDPSEYRVSELKESLITTAPSR 111
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; Pred. No. 0.14;
13; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 488;
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25561
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NUMBER OF SEQ ID NOS:
SEQ ID NO 24427
LENGTH: 384
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SEQ ID NO 25561
LENGTH: 133
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                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24427, Apparent No. 6551791
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-09-252-991A-24427
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APPLICANT: Marc J.
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Patent No. 6551795
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PRIOR PELING DATE: 1998-UZ-LO
PRIOR APPLICATION NUMBER: US 6
PRIOR APPLICATION DATE: 1998-07-27
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                      Local
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                                                                                                                                                                      Similarity
ASSRALLISALCACSAASTSMPATGAGARN--
                                     ANARAPTLRSATADNSEST-----GFKNVPDLRTDQP-KPPSKK------R 88
                                                                           TPPWPTLREKSNSSGSTSASSVRRSPRASSRTRRACSSPRC
                                                                                                                 TPPGP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTPSTPAIPTSSCRR-TVGIA----TAATSCSNPTKARTTRSASRVNISTDDSIPVSPT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTSSRP-LETPHCREIRIGIAGITITLSLCGCAN-ARAPTLRSATADN------
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                                                                                                                                                                    13.2%;
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                                                                                                                 -STVFRPPTSS----RPLETPHCREIRIGIAGITITLSLCGC 49
                                                                                                                                                                    Score 83.5; DB Pred. No. 0.22;
                                                                                                                                                       Mismatches
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---SOAPMKPPANRLAPTTOAPASISNR 153
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                                                                                                                                                       Indels
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US-09-252-991A-29784
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                                                                                Matches
                                                                                                                                                                                                                                          SEQ ID NO 29784
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                                                                                                                       Query Match
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                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                          TYPE: PRT
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                         LENGTH: 135
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Local Similarity 28.0%; Pred. No. 0.13;
hes 37; Conservative 14; Mismatches
                                                                                                      Local
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                                                                                                      Similarity
  PTSIR-----CRSISVACRARSIICPMCWPTTRRRPTRRTISCGSATGCIRQSRRCRST 69
                                      PTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLR----SATADNSESTGFKNV 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEKNPSSPSAGCTPTCSWTACGNASCTWPTSSWKVRIPNCCSTR----RASSTWPACSGS 132
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                                                                              12.9%; Score 81.5; DB ilarity 27.8%; Pred. No. 0.094; Conservative 12; Mismatches
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                                                                                                                       DB 2;
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
INUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10602
LENGTH: 766
TYPE: PAT
ORGANISM: Myxococcus xanthus
US-09-902-540-10602
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Search completed: April 20, 2006, 12:18:41 Job time : 48 secs
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US-09-902-540-10602
; Sequence 10602, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.8*; Score 81; DB 2; Length 766; Best Local Similarity 26.6*; Pred. No. 1.1; Matches 37; Conservative 19; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                      340 ALQQEDSADSAPTSQMPAFRARPGAPSAPHSSAPKPVPQRRPAEGGVALRGPSVAGNGSA 399
                                                                                                           456 QTQRFRSRPQRPGADGARV 474
                                                                                                                                                                                                                400 PKPAPQRRTSEAASPVSRTPRGGQDSAPAARTPRPRPTARQEVPAESESLD----EPSDL 455
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                                                                                                                                                                                                                                                                                                                                                                          3 ALQED-----TPPGPSTVFRP-----PTSSRPLETPHCREIRIGIAGITITLSLCGCA 50
                                                                                                                                                            KESLITTAPSRPRTARRRI 119
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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    on:
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Match
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Gapop 10.0 ,
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304.562 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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US-10-083-8498-10
US-10-083-8498-11
US-10-083-8498-11
US-10-083-8498-15
US-10-083-8498-15
US-10-083-8498-13
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US-10-083-8498-17
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Sequence 12, Appli
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Sequence 19, Appli
Sequence 7, Appli
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  RESULT 2
US-10-083-849B-1
; Sequence 1, Application US/10083849B
; Publication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009A1eborn, Mathieu
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	M B C - 1	CURP CURP PRIC PRIC NUME SOFI SEQ I	RESULT US-10-C ; Seque ; Publi ; GENER ; APPI ; APPI ; APPI ; APPI ; APPI	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ນ ກ
1 MNALQEDTPPGDSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA	IVAKE: MUTAGEN RITION: (1)(121) RITION: (1)(121) ER INFORMATION: single 83-8498-12 100. Match Local Similarity 100. Local Similarity 100.	ENT APPLICATION NUMBER: USAT FILING DATE: 2001-10 RATELING DATE: 2000-10-20 RAPPLICATION NUMBER: US RILING DATE: 2000-10-20 PROF SEQ ID NOS: 20 PARE: PatentIn version 3 NO 12 STH: 121 S: PRT NUISM: Chicken anemia vii		9 93.5 14.8 166 4 US 0 90 14.3 206 4 US 0 90 14.3 326 4 US 2 86.5 13.7 625 4 US 2 86 13.6 13.6 168 4 US 5 84 13.3 315 4 US 6 84 13.3 329 4 US 8 83 13.2 377 4 US 9 83 13.2 377 4 US 9 83 13.2 377 4 US 13.0 326 4 US	8 98 15 5 223 4 115
SRPLETPHCREIRIGIAGII	mutant T108A of Ap core 631; DB 4; red. No. 5e-55; Mismatches 0;	JS/10/083,849B 0-19 60/242,397) .1	orn, Mathieu of Apoptin	10-437-10-437-10-437-10-437-10-437-10-425-10	10-437-963
RIGIAGITITUSLCGCANARAPTLRSA 60	Apoptin Length 121; ; Indels 0; Gaps 0;	· ·	·	Sequence 13025, Sequence 120157, Sequence 157638, Sequence 15015, Sequence 150263, Sequence 160424, Sequence 66407, A Sequence 240302, Sequence 123418, Sequence 7, Appli Sequence 5639, Appl Sequence 5639, Appl Sequence 5639, Appl Sequence 57343, A Sequence 57343, A Sequence 57343, A Sequence 57343, A Sequence 57343, A Sequence 57343, A	Sequence 190571.

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TITLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ 1D NOS: 20
NUMBER OF SEQ 1D NOS: 3.1
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SEQ ID NO 16
LENGTH: 121
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                -10-083-8498-16
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TITLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR PILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
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                                                                                                                                                                                              NAME/KEY: MUTAGEN
LOCATION: (1)..(121)
OTHER INFORMATION: single point mutant T108E of Apoptin
                                                                                                                                                                                                                                                                         ORGANISM: Chicken anemia virus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC FEATURE
LOCATION: (1). (121) ·
OTHER INFORMATION: Apoptin (a small protein derived from chicken anemia virus) encod
OTHER INFORMATION: ed by pCMV-Vp3 and by GFP-Apoptin constructs
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                             MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
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MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
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99.2%;
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                                                                                    Score 626; DB 4; Length 121
Pred. No. 1.6e-54;
0; Mismatches 1; Indels
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Pred. No. 1.2e-54;
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US-10-083-849B-18
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                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 121
                                                                                                                                                                                                                                                                                           Sequence 19, Application US/10083849B Publication No. US20030199009A1
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Best Local &
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                                                     PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
                                                                                                                  FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
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NAME/KEY: MUTAGEN
LOCATION: (1)..(121)
OTHER INFORMATION: c
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CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
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APPLICANT: Mumberg, Dominik
APPLICANT: Domner, Peter
TITLE OF INVENTION: Modifications of Apoptin
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APPLICANT: No. US20030199009A1eborn,
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Pred. No. 1.6e-54;
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Publication No. US20050100552A1
GENERAL INFORMATION:
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LOCATION: (1)..(121)
OTHER INFORMATION: double point mutant T106A108A of Apoptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Chicken anemia virus FEATURE:
                        APPLICATION NUMBER: US 08/030,335
FILING DATE: 08-MARCH-1993
APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JULY-1993
'APPLICATION NUMBER: PCT/NL 91/00165
FILING DATE: 11-SEPTEMBER-1991
APPLICATION NUMBER: NL 9002008
FILING DATE: 11-SEPTEMBER-1990
APPLICATION NUMBER: NL 9002008
FILING DATE: 11-SEPTEMBER-1990
APPLICATION NUMBER: 32.970
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV.003.01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 926-6205
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/454,121

FILING DATE: 30-NOVEMBER-1995

APPLICATION NUMBER: PCT/NL 94/00168

FILING DATE: 19-JULY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER RADALLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0,
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
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And Uses Based On The Viral Proteins VP1,
Sequences Of That Virus Coding Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/740,676
FILING DATE: 18-Dec-2000
CLASSIFICATION: «Unknown»
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                ELEPHONE: (650) 926-6205
ELEPAX: (650) 424-8760
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99.2%;
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Pred. No. 1.6e-54;
0; Mismatches 1
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                                  121 F 121
121 L 121
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Sequence 2, Application US/10083849B Publication No. US20030199009A1 GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, APPLICANT: Rohn, Jennifer Leigh
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE OTHER INFORMATION: Differs from Apoptin protein encoded by pCMV-Vp3 and by GFP-Apop OTHER INFORMATION: in constructs by replacement of the arginine residue at position OTHER INFORMATION: 116 with a lysine residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 121
TYPE: PRT
ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MUTAGEN
LOCATION: (1)...(121)
OTHER INFORMATION: Apoptin protein encoded by pIRESneo alanine mutants
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                         61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRRIR 120
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TADNSESTGFKNVPDLKTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRRIR 120
                                                                                          MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
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milarity 98.3%;
Conservative
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Pred. No. 2.5e-54;
1; Mismatches 1
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Pred. No. 2.5e-54;
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JS-10-083-849B-10

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APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 121
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; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(121)
; OTHER INFORMATION: single point mutant T107A of Apoptin
US-10-083-849B-11
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TITLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
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PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
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LOCATION: (1)..(121)
OTHER INFORMATION: single point mutant T106A of Apoptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Chicken anemia virus
                                                                                                                                    ORGANISM: Chicken anemia virus
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US-10-083-849B-15
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APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
                                                                                                             GENERAL INFORMATION:
APPLICANT: No. US20
                                                                                                                                                 Sequence 15, Application US/10083849B Publication No. US20030199009A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn' version 3.1 SEQ ID NO 14
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Best Local Similarity
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APPLICANT: Donner, Peter

TITLE OF INVENTION: Modifications of Apoptin

FILE REFERENCE: 2906-4996.1
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CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MUTAGEN
                 PPLICANT: Mumberg, Dominik
PPLICANT: Donner, Peter
ITLE OF INVENTION: Modifications of Apoptin
ILE REFERENCE: 2906-4996.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Chicken anemia virus
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                                                                                          Rohn, Jennifer Leigh
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                                                                                                               US20030199009Aleborn, Mathieu
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Pred. No. 4.9e-54;
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Best Local S
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LENGTH: 121
TYPE: PRT
ORGANISM: Chicken anemia virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
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PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                    LENGTH: 121
TYPE: PRT
ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                             FEATURE: "TRATURE: NAME/KEY: MUTAGEN
LOCATION: (1)..(121)
OTHER INFORMATION: single point mutant P109A of Apoptin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
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WINDER OF SEQ ID NOS: 20
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OTHER INFORMATION: single point mutant T107E of Apoptin
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NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLICANT: Donner, Peter
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                                   61 TADNSESTGFKNVPDLRTDOPKPPSKKRSCDPSEYRVSELKESLITTTASRPRTARRRIR
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                                                                                                           MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
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Pred. No.
                                                                                                                                                                                                     Score 619; DB 4; Length 121; Pred. No. 7.8e-54;
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US-10-083-849B-17
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/ ORGANISM: Chicken anemia virus
US-10-488-363-2
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                                                                                                                                                                 SEQ ID NO 17
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Best Local Similarity
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LENGTH: 786
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Publication No.
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                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT EILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                               APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
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PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: 60/317,239
PRIOR FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 2
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CURRENT FILING DATE: 2004-03-02
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             OTHER INFORMATION: double point mutation T106A107A of Apoptin
                                         NAME/KEY: MUTAGEN LOCATION: (1)..(1)
                                                                              TYPE: PRT
ORGANISM: Chicken anemia virus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT: No. US20030199009Aleborn, Mathieu.
PPLICANT: Rohn, Jennifer Leigh
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                                                                                                                                           ENGTH: 121
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98.3%;
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Pred. No. 7.2e-53;
0; Mismatches
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Query Match

97.8%;

Score 617;

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RESULT 15
US-10-738-423-58
; Sequence 58, Application US/10738423
; Publication No. US20040229338A1
; GENERAL INFORMATION:
Search completed: April 20, 2006, 12:32:20 Job time : 167 secs
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; TYPE: PRT
; ORGANISM: Bacteriophage
US-10-738-423-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 61
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                 Query Match 97.6%; Score 616; DB 5; Length 134; Best Local Similarity 97.5%; Pred. No. 1.8e-53; Matches 118; Conservative 1; Mismatches 2; Indels
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
FILE REFERENCE: 8002-059
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: US/09/645,415
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/157,581
PRIOR APPLICATION NUMBER: 60/157,581
PRIOR PILING DATE: 1999-10-04
PRIOR PILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
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Clairmont, C.
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Maximum DB
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Listing first 45 summaries
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2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/US03_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-204-980-16
US-11-204-980-17
US-11-096-568A-17740
US-11-096-568A-24347
US-11-096-568A-24535
US-11-096-568A-115924
US-11-096-568A-1120
US-11-096-568A-1120
US-11-096-568A-1294
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US-11-096-568A-26546
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US-11-124-368A-291
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58, Appl

60, Appl

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21, Appl

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21535, Appl

215924, Appl

26545, Appl

26545, Appl

289, Appl

290, Appl

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291, Appl

2
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RESULT 2 US-11-082-544-58

Sequence 58, Application US/11082544 Publication No. US20050249706A1

GENERAL INFORMATION:
APPLICANT: Bermudes, G.
APPLICANT: King, I.
APPLICANT: Clairmont, C.

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ion US/11204: 066057652A1 Michael Michael , Destin , Destin , Destin , METHODS FOR AGENTS AND 17-196001 17-196001 18-196001 19-196001 2004-08-13 S: 19 or Windows Vo 2004-08-13 S: 19 98.9%; y 98.3%; rvative 1; ppGpSTVFRPPTS ppG	954 198 273 273 273 273 273 273 276 278 286 286 286 287 287 287 298 298 298 298 298 298 298 298 298 298
ALIGNMENTS 11204980 152A1 152A1 16 17 18 19 19 10 10 10 11 10 10 11 11 11 11 11 11 11	7 US-11-188-298-16512 7 US-11-096-568A-9882 7 US-11-096-568A-1837 7 US-11-124-368A-187 7 US-11-096-568A-2109 7 US-11-096-568A-25420 US-11-096-568A-25420 US-11-096-568A-25420 US-11-096-568A-25420 US-11-096-568A-25420 US-11-096-568A-25419 7 US-11-096-568A-25419 7 US-11-096-568A-25419 7 US-11-096-568A-25419 7 US-11-096-568A-25419 7 US-11-096-568A-25419 7 US-11-096-568A-25419 8 US-10-242-586-54 6 US-10-243-116-54 6 US-10-243-116-54 6 US-10-243-189-54 6 US-10-243-189-54
ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ACIDER G. CON: MICHAel MAID. Destin CON: METHODS FOR IDENTIFYING THERAPEUTIC CON: METHODS FOR IDENTIFYING DISEASE O7917-196001 CON: METHODS FOR IDENTIFYING DISEASE O7917-196001 ATE: 2005-08-15 AN NUMBER: US 60/601,494 E. 2004-08-13 INOS: 19 Q. for Windows Version 4.0 EDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60 EDTPPGPSTVFRPPTSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60 EDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60 EDTPPGPSTVFRPTAMPT 121 ENTANTAMPT 121 ENTANT	2 Sequence 16512, A Sequence 9882, Ap 37 Sequence 11837, A Sequence 1187, App 09 Sequence 122109, A 15 Sequence 122115, A Sequence 25421, Ap 21 Sequence 25420, A 20 Sequence 25420, A Sequence 25421, Ap 19 Sequence 26419, A Sequence 26984, A 19 Sequence 27, Appl Sequence 54, Appl

ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES

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CURRENT APPLICATION NUMBER: US/11/082,544

CURRENT PILING DATE: 2005-03-17

PRIOÙ APPLICATION NUMBER: US/09/645,415

PRIOR APPLICATION NUMBER: 60/157,581

PRIOR APPLICATION NUMBER: 60/157,637

PRIOR APPLICATION NUMBER: 60/157,637

PRIOR APPLICATION NUMBER: 60/157,637

PRIOR APPLICATION NUMBER: 60/157,637

PRIOR FILING DATE: 1999-10-04
                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 60
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                                                                        Matches 118;
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FILE REPERENCE: 8002-059

CURRENT APPLICATION NUMBER: US/11/082,544

CURRENT FILING DATE: 2005-03-17

PRIOR APPLICATION NUMBER: US/09/645,415

PRIOR PELING DATE: 2000-08-24

PRIOR PILING DATE: 2000-08-24

PRIOR PILING DATE: 1099-10-04

PRIOR FILING DATE: 1099-10-04
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                      ORGANISM: Bacteriophage
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108 118; Conservative
                                                                                                Local Similarity
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MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
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                                                                          Conservative
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97.5%;
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                                                                                                Score 616; DB 7; Length 140; Pred. No. 1.5e-56;
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APPLICANT: Green, Michael
APPLICANT: Healman, Destin
APPLICANT: Healman, Destin
APPLICANT: Teodoro, Jose G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING THERAPEUTIC
TITLE OF INVENTION: AGENTS AND FOR TREATING DISEASE
FILE REFERENCE: 07917-196001
CURRENT APPLICATION NUMBER: US/11/204,980
CURRENT FILING DATE: 2005-08-15
PRIOR APPLICATION NUMBER: US 60/601,494
PRIOR FILING DATE: 2004-08-13
NUMBER OF SEQ ID NOS: 19
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Query Match 31.1%;
Best Local Similarity 95.0%;
Matches 38; Conservative
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CURRENT APPLICATION NUMBER: US/11/204,980
CURRENT FILING DATE: 2005-08-15
PRIOR APPLICATION NUMBER: US 60/601,494
PRIOR PRIOR APPLICATION NUMBER: US 60/601,494
PRIOR FILING DATE: 2004-08-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PASCSEQ for Windows Version 4.0
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APPLICANT: Heilm
APPLICANT: Teodo
                                                                                                                                      LENGTH: 40
                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 80
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 ESLITTAPSRPRTARRIRL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 L 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 г 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 TADNSENTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRCIR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 ITLSLCGCANARAPTLRSATADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TADNSESTGFKNVPDLRTDQPKPPSKKKSCDPSEYRVSELKESLITTAPSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.0%;
Similarity 97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heilman, Destin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLSLCGCANARAPTLRSATADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/11204980
No. US20060057652A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Destin
    Score 196; DB 7;
Pred. No. 7.7e-14;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 404; DB 7
Pred. No. 6e-35;
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                                              Length 40;
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                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 24347
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24347, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 17740
LENGTH: 183
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                                                                                                                                                                                    11-096-568A-24347
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)..(319)
OTHER INFORMATION: Ceres Seq. ID no. 12434866
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION: Sequence-Determined DNA Fragments and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alexandrov, Nickolai et al
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OTHER INFORMATION: Ceres Seq. ID no. 12360044
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                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                 191
                                                                                  5
64 NSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 PASSR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 NSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                      319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 26.9
31; Conservative
                                                                                  PGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCG-----CANARAPTLRSATAD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPPTPPP--QPPSPEGPPHSPAARRR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAP----TLRSATAD 63
                                                 PSPSSPTAPPSPTR----CRSSTTARASASSARRLCSRSSSTMAASSSRSTSSAATSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRRIRL
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                                                                                                                   Conservative
                                                                                                                               13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.7%;
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                                                                                                                14;
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                                                                                                                               Score 86; DB Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86.5; DB
Pred. No. 0.092;
9; Mismatches
                                                                                                                Mismatches
                                                                                                                                                 DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7;
                                                                                                                 41;
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                                                                                                                                               Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 183;
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --RTTPSRPRPLARTRR 107
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                                                                                                                 30;
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                                                                                                                                                                    Matches
                                                                                                                                                                                                  Query Match
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LENGTH: 300
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                                                                                                                                                                                                                                                     OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                         ID NO 11657
                                                                                                                                                                                    Local
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                                                                                                                                                                    39;
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                                                                                                                                                                                    Similarity
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Sequence 11657, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27037, Application US/11096568A
Publication No. US20060048240A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Sequence-Determined TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Alexandrov, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)..(493)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(300)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: Ceres Seq.
                                       180 RSAPAASATTRTTAPTTTRASAATSRTPPSPRSTSSPTGPSSSRSPSPTSPSSPSPSPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 PSPSSPTAPPSPTR-----CRSSTTARASASSARRLCSRSSSTMAASSSRSTSSAATSL
                                                                                                                      128 SPPPPRT--RPSASSTPSRRPSTR--ASGPSG----ASTSGPSSPSAATRRSRPSAARPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 ASSAVACPTCPPRMTHRPRDPS----PS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 PGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCG-----CANARAPTLRSATAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 NSESTGFKNVPDLRTDOPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRR 118
                                                                                                                                                                8 TPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRS------
EYRVSELKESLITTAPSRPRTARR 117
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                               Ceres Seq.
                                                                                                                                                                                                                             12.2%;
                                                                                 ---ATADNSESTGFKNVPDLR-TDQPKPPSKKRSCDP---
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Pred. No.
                                                                                                                                                                                                                             Score 77; DB 7; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                            ID no. 15219800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID no. 13666262
                                                                                                                                                                                                       Mismatches
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                                       239
                                                                               93
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                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 15924
TENTIFIC 238
                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15924, Application US/11096568A Publication No. US20060048240A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 24535
LENGTH: 319
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APPLICANT: Alexandrov, Nickolai et al.
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Publication No. US20060048240A1
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                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)..(238)
OTHER INFORMATION: Ceres Seq. ID
                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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OTHER INFORMATION: Ceres Seq. ID
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LOCATION: (1)..(319)
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                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 CPSTSPRACRSARGSAPPRPPPPPPPPPPPPSSARA----SAATTSSSRGSSRRR 205
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                                 56 TLRSATADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTA 115
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TC-GASSSTGSSRSPRSTSSSRTRSTSPSLMSTASSPSTRSAVTSCSSLALPPCSLPRSS
                                                                   OPTPLSPRRRAPWRPPTSSSPGPTPPTSTPTSAPWRWIR---
                                                                                                      EDTPPGP--STVFRPPTSSRPLETPHC-----REIRIGIAGITITLSLCGCANARAP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ESTGFKNVPDLR----TDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPSPS----PPSHPRP--APTSPSASLGTRSAT--
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                                                                                                                                            Conservative
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                                                                                                                                                           11.98;
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                                                                                                                                                            Score 75; I
Pred. No. 1
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                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                  no. 12349596
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                                                                                                                                                                             DB 7; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7;
                                                                                                                                            65;
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                                                                                                                                            Indels
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                                                                                                                                            14;
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                                                      SOFTWARE: Pa
SEQ ID NO 137
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; TYPE: PRT ; ORGANISM: Homo sapiens US-11-069-642-137
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                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 10/232,758
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 10/422,536
PRIOR FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 09/800,770
PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 60/187,130
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LENGTH: 267
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CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                PRIOR FILING DATE: 2000-03-06 NUMBER OF SEQ ID NOS: 168 SOFTWARE: PatentIn version 3.
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/069,642
CURRENT FILING DATE: 2005-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PRAY, TODD R.
APPLICANT: KINSELLA, TODD M.
APPLICANT: BENNETT, MARK K.
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: RIGL-022CIP3
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LOCATION: (1)..(267)
OTHER INFORMATION: Ceres Seq. ID no. 13600172
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ORGANISM: Zea mays subsp.
FEATURE:
                                                                            LENGTH: 491
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11.7%; Score 74; 1 26.2%; Pred. No. 5

DB 7;

Length 491

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; LOCATION: (1)..(554)
; OTHER INFORMATION: Ceres Seq.
US-11-096-568A-17691
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                             Sequence 26346, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 26546
LENGTH: 164
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Best Local Similarity
Matches 34; Conserv
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Best Local Similarity
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LENGTH: 554
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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ORGANISM: Zea mays subsp. mays
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Best Local Similarity
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NAME/KEY: misc_feature
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TON: Cey
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LOCATION: (53) ...(53)
OTHER INFORMATION: Xaa is
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OTHER INFORMATION: Xaa
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NAME/KEY: misc_feature
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                                                      119 TASPSRPCATSATPSSPCAVRSCPP 143
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                                                                                                          67 SRLWRPPCGASTSRPFAPPWRRRCRRPCGGWECTGRCCSSACCSPGSPT---
                                                                              TGFKNVPDLRTDQPKPPSKKRSCDP 92
                                                                                                                                  STVFRPP---TSSRPLETPHCREIRIGIAGITITLSLC--GCANARAPTLRSATADNSES 67
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Pred. No. 1.8;
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